

1 MMQKLQMYVY 10  
 1 M I QKPQMYVY 10  
 1 -M QKLQ L CVY 9  
 1 -M QKLQ L CVY 9  
 1 -M QKLQ I SVY 9  
 1 -M QKLQ I YVY 9  
 1 -M QKLQ I FVY 9  
 1 -M QKLA VYVY 9  
 1 -M Q I LA VYVY 9  
 1 -MH FTQ-----VL 7

31 EENVEKEGLC 40  
 31 EANVEKEGLC 40  
 30 KENVEKEGLC 39  
 30 KENVEKEGLC 39  
 30 KENVEKEGLC 39  
 30 KENVEKEGLC 39  
 30 KENVEKKGLC 39  
 30 TENAEKDGLC 39  
 30 TENAEKDGLC 39  
 31 STAT EES ELC 40

61 ILSKLRLETA 70  
 61 ILSKLRLETA 70  
 60 ILSKLRLETA 69  
 60 ILSKLRLETA 69  
 60 ILSKLRLETA 69  
 60 ILSKLRLETA 69  
 60 ILSKLRLETA 69  
 60 ILSKLRLEQA 69  
 60 ILSKLRLEQA 69  
 61 ILSKLRLEQA 70

91 LI DQYDVQRD 100  
 91 LI DQYDVQRD 100  
 90 LI DQYDVQRD 99  
 90 LI DQYDVQRD 99  
 90 LI DQYDVQRD 99  
 90 LI DQYDVQRD 99  
 90 LI DQYDVQRD 99  
 90 LI DQYDVQRD 99  
 90 LI DQYDVQRD 99  
 90 LI DQYDVQRD 99  
 91 LLDQYDVLGD 100

11 IYLFMLIAAG 20  
 11 IYLFVLI AAG 20  
 10 IYLFMLI VAG 19  
 10 IYLFMLI VAG 19  
 10 IYLFMLI VAG 19  
 10 IYLFMLI VAG 19  
 10 IYLFMLI VAG 19  
 10 IYLFMLI VAG 19  
 10 IYLFMQ I AVD 19  
 10 IYLFMQ I LVH 19  
 8 ISLS VL I ACG 17

41 NACA WRQNTR 50  
 41 NACA WRQNTR 50  
 40 NACT WRQNTK 49  
 40 NACT WRQNTK 49  
 40 NACL WRE NTT 49  
 40 NACMWRQNTK 49  
 40 NACL WRQNNK 49  
 40 NACT WRQNTK 49  
 40 NACT WRQNTK 49  
 40 NACT WRQNTK 49  
 41 S TCE FRQHSK 50

71 PNISKDA IRQ 80  
 71 PNISKDA IRQ 80  
 70 PNISKDV IRQ 79  
 70 PNISKDA IRQ 79  
 70 PNISKDA IRQ 79  
 70 PNISKDA IRQ 79  
 70 PNISKDA IRQ 79  
 70 PNISKDA IRQ 79  
 70 PNISRDV IKQ 79  
 70 PNISRDV IKQ 79  
 71 PNISRDVVKQ 80

101 DS SDGSLEDD 110  
 101 DS SDGSLEDD 110  
 100 DS SDGSLEDD 109  
 100 DS SDGSLEDD 109  
 100 AS SDGSLEDD 109  
 100 DS SDGSLEDD 109  
 100 DS SDGSLEDD 109  
 100 DS SDGSLEDD 109  
 100 DS SDGSLEDD 109  
 100 DS SDGSLEDD 109  
 101 DSKDGAVEED 110

21 PV-----DLNEGSR 30 Mouse  
 21 PV-----DLNEDSR 30 Rat  
 20 PV-----DLNENSEQ 29 Human  
 20 PV-----DLNENSEQ 29 Baboon  
 20 PV-----DLNENSEQ 29 Bovine  
 20 PV-----DLNENSEQ 29 Porcine  
 20 PV-----DLNENSEQ 29 Ovine  
 20 PV-----ALDGSSQP 29 Chicken  
 20 PV-----ALDGSSQP 29 Turkey  
 18 PVGYGDITAHQQP 30 Zebrafish

51 YS RI E AIKIQ 60 Mouse  
 51 YS RI E AIKIQ 60 Rat  
 50 SS RI E AIKIQ 59 Human  
 50 SS RI E AIKIQ 59 Baboon  
 50 SS RLE AIKIQ 59 Bovine  
 50 SS RLE AIKIQ 59 Porcine  
 50 SS RLE AIKIQ 59 Ovine  
 50 SS RI E AIKIQ 59 Chicken  
 50 SS RI E AIKIQ 59 Turkey  
 51 LM RLHAISQ 60 Zebrafish

81 LLPRAPPLRE 90 Mouse  
 81 LLPRAPPLRE 90 Rat  
 80 LLPKAPPLRE 89 Human  
 80 LLPKAPPLRE 89 Baboon  
 80 LLPRAPPLRE 89 Bovine  
 80 LLPRAPPLRE 89 Porcine  
 80 LLPRAPPLRE 89 Ovine  
 80 LLPRAPPLQE 89 Chicken  
 80 LLPRAPPLQE 89 Turkey  
 81 LLPRAPPLQQ 90 Zebrafish

111 DYH ATTET I I 120 Mouse  
 111 DYH ATTET I I 120 Rat  
 110 DYH ATTET I I 119 Human  
 110 DYH ATTET I I 119 Baboon  
 110 DYH ARTETV I I 119 Bovine  
 110 DYH ATTET I I 119 Porcine  
 110 DYH VTTETV I I 119 Ovine  
 110 DYH ATTET I I 119 Chicken  
 110 DYH ATTET I I 119 Turkey  
 111 DEH ATTET IM 120 Zebrafish

FIG. 1A

121 TMPTESDFLM 130	131 QADGKPKCCF 140	141 FKFSSKIQYN 150 Mouse
121 TMPTESDFLM 130	131 QADGKPKCCF 140	141 FKFSSKIQYN 150 Rat
120 TMPTESDFLM 129	130 QVDGKPKCCF 139	140 FKFSSKIQYN 149 Human
120 TMPTESDFLM 129	130 QVDGKPKCCF 139	140 FKFSSKIQYN 149 Baboon
120 TMPTESDLL T 129	130 QVEGKPKCCF 139	140 FKFSSKIQYN 149 Bovine
120 TMPTESDLLM 129	130 QVEGKPKCCF 139	140 FKFSSKIQYN 149 Porcine
120 TMPTESDLL A 129	130 EVQEKPKCCF 139	140 FKFSSKIQHN 149 Ovine
120 TMPTESDFL V 129	130 QMEGKPKCCF 139	140 FKFSSKIQYN 149 Chicken
120 TMPTESDFL V 129	130 QMEGKPKCCF 139	140 FKFSSKIQYN 149 Turkey
121 TMATEPDPI V 130	131 QVDRKPKCCF 140	141 FS FSPKIQAN 150 Zebrafish
151 KVVKAQLW IY 160	161 LRP VKTPTTV 170	171 FVQILRLIKP 180 Mouse
151 KVVKAQLW IY 160	161 LRAVKTPTTV 170	171 FVQILRLIKP 180 Rat
150 KVVKAQLW IY 159	160 LRP VETPTTV 169	170 FVQILRLIKP 179 Human
150 KVVKAQLW IY 159	160 LRP VETPTTV 169	170 FVQILRLIKP 179 Baboon
150 KLVKAQLW IY 159	160 LRP VKTPATV 169	170 FVQILRLIKP 179 Bovine
150 KVVKAQLW IY 159	160 LRP VKTPTTV 169	170 FVQILRLIKP 179 Porcine
150 KVVKAQLW IY 159	160 LRP VKTPTTV 169	170 FVQILRLIKP 179 Ovine
150 KVVKAQLW IY 159	160 LRQVQKPTTV 169	170 FVQILRLIKP 179 Chicken
150 KVVKAQLW IY 159	160 LRQVQKPTTV 169	170 FVQILRLIKP 179 Turkey
151 R I VRAQLWVH 160	161 LRP AEEATTV 169	170 FLQISRLM-P 179 Zebrafish
181 MKDGTRYTGI 190	191 RSLKLDMSPG 200	201 TGIWQSIDVK 210 Mouse
181 MKDGTRYTGI 190	191 RSLKLDMSPG 200	201 TGIWQSIDVK 210 Rat
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Human
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Baboon
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Bovine
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Porcine
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Ovine
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Chicken
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Turkey
180 V KDGGRHR-I 188	189 RSLK IDV NAG 198	199 VTSWQSIDVK 208 Zebrafish
211 TVLQNWLKQP 220	221 ESNLGIEIKA 230	231 LD ENGHDLAV 240 Mouse
211 TVLQNWLKQP 220	221 ESNLGIEIKA 230	231 LD ENGHDLAV 240 Rat
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Human
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Baboon
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Bovine
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Porcine
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Ovine
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 FD ETGRDLAV 239 Chicken
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 FD ENGRDLAV 239 Turkey
209 QVLTVWLKQP 218	219 ETNRGIEINA 228	229 YDAKGNDLAV 238 Zebrafish

FIG. 1B

241 TFPGPGE DGL 250	251 NPFLEV K VTD 260	261 TPKRSRRDFG 270 Mouse
241 TFPGPGE DGL 250	251 NPFLEV K VTD 260	261 TPKRSRRDFG 270 Rat
240 TFPGPGE DGL 249	250 NPFLEV K VTD 259	260 TPKRSRRDFG 269 Human
240 TFPGPGE DGL 249	250 NPFLEV K VTD 259	260 TPKRSRRDFG 269 Baboon
240 TFPEPGE DGL 249	250 TPFLEV K VTD 259	260 TPKRSRRDFG 269 Bovine
240 TFPGPGE DGL 249	250 NPFLEV K VTD 259	260 TPKRSRRDFG 269 Porcine
240 TFPEPGE E GL 249	250 NPFLEV K VTD 259	260 TPKRSRRDFG 269 Ovine
240 TFPGPGE DGL 249	250 NPFLEV R VTD 259	260 TPKRSRRDFG 269 Chicken
240 TFPGPGE DGL 249	250 NPFLEV R VTD 259	260 TPKRSRRDFG 269 Turkey
239 TSTETGE DGL 248	249 LPFMEV KI SE 258	259 GPKRIR RDSG 268 Zebrafish
271 LDCDEHSTES 280	281 RCCRYPLTV D 290	291 FEAFGWDWII 300 Mouse
271 LDCDEHSTES 280	281 RCCRYPLTV D 290	291 FEAFGWDWII 300 Rat
270 LDCDEHSTES 279	280 RCCRYPLTV D 289	290 FEAFGWDWII 299 Human
270 LDCDEHSTES 279	280 RCCRYPLTV D 289	290 FEALGWDWII 299 Baboon
270 LDCDEHSTES 279	280 RCCRYPLTV D 289	290 FEAFGWDWII 299 Bovine
270 LDCDEHSTES 279	280 RCCRYPLTV D 289	290 FEAFGWDWII 299 Porcine
270 LDCDEHSTES 279	280 RCCRYPLTV D 289	290 FEAFGWDWII 299 Ovine
270 LDCDEHSTES 279	280 RCCRYPLTV D 289	290 FEAFGWDWII 299 Chicken
270 LDCDEHSTES 279	280 RCCRYPLTV D 289	290 FEAFGWDWII 299 Turkey
269 LDCDEN SSES 278	279 RCCRYPLTV D 288	289 FEDFGWDWII 298 Zebrafish
301 APKRYKANYC 310	311 SGECE FV FLQ 320	321 KYPHTHLVHQ 330 Mouse
301 APKRYKANYC 310	311 SGECE FV FLQ 320	321 KYPHTHLVHQ 330 Rat
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Human
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Baboon
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Bovine
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Porcine
300 APKRYKANYC 309	310 SGECE FL FLQ 319	320 KYPHTHLVHQ 329 Ovine
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Chicken
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Turkey
299 APKRYKANYC 308	309 SGECDYMYLQ 318	319 KYPHTHLV NK 328 Zebrafish
331 ANPRGSAGPC 340	341 CTPTKMSPIN 350	351 MLYFNGKEQI 360 Mouse
331 ANPRGSAGPC 340	341 CTPTKMSPIN 350	351 MLYFNGKEQI 360 Rat
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Human
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Baboon
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGGEGQI 359 Bovine
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Porcine
330 ANPKGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Ovine
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Chicken
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Turkey
329 ASPRGTAGPC 338	339 CTPTKMSPIN 248	349 MLYFNGKEQI 359 Zebrafish

FIG. 1C

361 IYGKIPAMVV 370	371 DRCGCS 376 Mouse
361 IYGKIPAMVV 370	371 DRCGCS 376 Rat
360 IYGKIPAMVV 369	370 DRCGCS 375 Human
360 IYGKIPAMVV 369	370 DRCGCS 375 Baboon
360 IYGKIPAMVV 369	370 DRCGCS 375 Bovine
360 IYGKIPAMVV 369	370 DRCGCS 375 Porcine
360 IYGKIPGMVV 369	370 DRCGCS 375 Ovine
360 IYGKIPAMVV 369	370 DRCGCS 375 Chicken
360 IYGKIPAMVV 369	370 DRCGCS 375 Turkey
359 IYGKIP SMVV 368	369 DRCGCS 374 Zebrafish

FIG. 1D

			10				20				30				40	
GGA	TCC	CGT	TCT	CGT	CGC	GAC	TTT	GGT	CTG	GAC	TGC	GAC	GAA	CAT		
Gly	Ser	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His		
			50												60	
TCT	ACC	GAA	AGA	TCT												
Ser	Thr	Glu	Arg	Ser												

FIG. 2

			10				20				30				40	
GGA	TCC	TCT	CGT	TGC	TGT	CGC	TAT	CCG	CTG	ACC	GTT	GAC	TTC	GAA		
Gly	Ser	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu		
			50													
AGA	TCT															
Arg	Ser															

FIG. 3

			10				20				30				40	
GGA	TCC	TTC	GAA	GCT	TTT	GGT	TGG	GAC	TGG	ATC	ATT	GCA	CCG	AAA		
Gly	Ser	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys		
			50													
CGT	TAT	AGA	TCT													
Arg	Tyr	Arg	Ser													

FIG. 4

10                      20                      30                      40  
 GGA TCC AAA CGT TAT AAA GCT AAC TAT TGC TCT GGT GAA TGC GAA  
 Gly Ser Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu

50  
 TTC AGA TCT  
 Phe Arg Ser

FIG. 5

10                      20                      30                      40  
 GGA TCC GAA TTC GTT TTC CTG CAG AAA TAT CCG CAT ACC CAT CTG  
 Gly Ser Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu

50                      60                      70  
 GTT CAT CAG GCT AAC CCG CGT AGA TCT  
 Val His Gln Ala Asn Pro Arg Arg Ser

FIG. 6

10                      20                      30                      40  
 GGA TCC GCT GGT CCG TGC TGT TAT CCG ACC AAA ATG TCT CCG ATC  
 Gly Ser Ala Gly Pro Cys Cys Tyr Pro Thr Lys MET Ser Pro Ile

50                      60                      70                      80  
 AAC ATG CTG TAT TTC AAC GGT GAA TGC CAG AGA TCT  
 Asn MET Leu Tyr Phe Asn Gly Glu Cys Gln Arg Ser

FIG. 7

10                      20                      30                      40  
 GGA TCC GAA TGC CAG ATC ATT TAT TGC AAA ATC CCG GCT ATG GTT  
 Gly Ser Glu Cys Gln Ile Ile Tyr Cys Lys Ile Pro Ala MET Val

50                      60                      70  
 GTA GAC CGT TGC GGT TGT TCT AGA TCT  
 Val Asp Arg Cys Gly Cys Ser Arg Ser

FIG. 8

10                      20                      30                      40  
 GGA TCC GAA CAG AAA GAA AAC GTT GAA AAA GAA GGT CTG TGC AAC  
 Gly Ser Glu Gln Lys Glu Asn Val Glu Lys Glu Gly Leu Cys Asn

50                      60  
 GCT TGC CTG TGG AGA TCT  
 Ala Cys Leu Trp Arg Ser

FIG. 9

10                      20                      30                      40  
 GGA TCC CAT GAC CTG GCT GTT ACC TTC CCG GAA CCG GGT GAA GAC  
 Gly Ser His Asp Leu Ala Val Thr Phe Pro Glu Pro Gly Glu Asp

50                      60  
 GGT CTG ACC AGA TCT  
 Gly Leu Thr Arg Ser

FIG. 10

			10				20				30				40			
			↓				↓				↓				↓			
GGA	TCC	ACC	CCG	TTC	CTG	GAA	GTT	AAA	GTT	ACC	GAC	ACT	CCG	AAA				
Gly	Ser	Thr	Pro	Phe	Leu	Glu	Val	Lys	Val	Thr	Asp	Thr	Pro	Lys				
			50												60			
			↓												↓			
CGT	TCT	CGT	AGA	TCT														
Arg	Ser	Arg	Arg	Ser														

FIG. 11

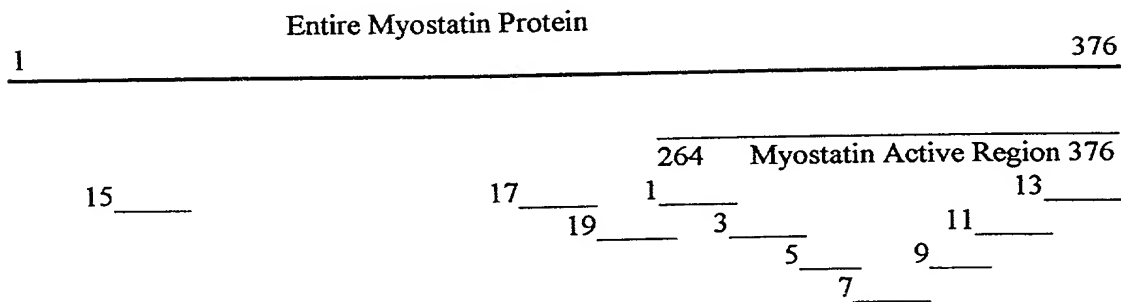


FIG. 12



		10				20				30				40					
GGA	TCC	CGT	TCT	CGT	CGC	GAC	TTT	GGT	CTG	GAC	TGC	GAC	GAA	CAT					
Gly	Ser	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His					
		50				60				70				80					90
TCT	ACC	GAA	AGA	TCC	TCT	CGT	TGC	TGT	CGC	TAT	CCG	CTG	ACC	GTT					
Ser	Thr	Glu	Arg	Ser	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val					
		100				110				120				130					
GAC	TTC	GAA	GCT	TTT	GGT	TGG	GAC	TGG	ATC	ATT	GCA	CCG	AAA	CGT					
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg					
		140				150				160				170					180
TAT	AGA	TCC	AAA	CGT	TAT	AAA	GCT	AAC	TAT	TGC	TCT	GGT	GAA	TGC					
Tyr	Arg	Ser	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys					
		190				200				210				220					
GAA	TTC	GTT	TTC	CTG	CAG	AAA	TAT	CCG	CAT	ACC	CAT	CTG	GTT	CAT					
Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His					
		230				240				250				260					270
CAG	GCT	AAC	CCG	CGT	AGA	TCC	GCT	GGT	CCG	TGC	TGT	TAT	CCG	ACC					
Gln	Ala	Asn	Pro	Arg	Arg	Ser	Ala	Gly	Pro	Cys	Cys	Tyr	Pro	Thr					
		280				290				300				310					
AAA	ATG	TCT	CCG	ATC	AAC	ATG	CTG	TAT	TTC	AAC	GGT	GAA	TGC	CAG					
Lys	<u>MET</u>	Ser	Pro	Ile	Asn	<u>MET</u>	Leu	Tyr	Phe	Asn	Gly	Glu	Cys	Gln					
		320				330				340				350					360
ATC	ATT	TAT	TGC	AAA	ATC	CCG	GCT	ATG	GTT	GTA	GAC	CGT	TGC	GGT					
Ile	Ile	Tyr	Cys	Lys	Ile	Pro	Ala	<u>MET</u>	Val	Val	Asp	Arg	Cys	Gly					
		370																	
TGT	TCT	AGA	TCT																
Cys	Ser	Arg	Ser																

FIG. 13

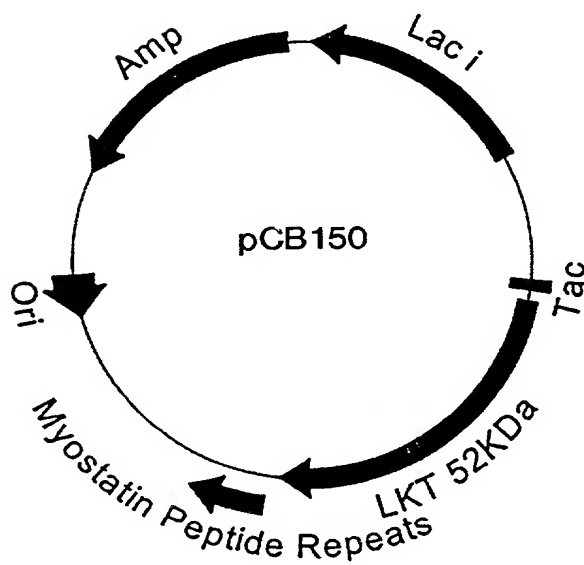


FIG. 14

1870                    1880                    1890                    1900                    1910  
 |                    |                    |                    |                    |  
 ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA  
 MET Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys

1920                    1930                    1940                    1950  
 |                    |                    |                    |  
 AAA ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA  
 Lys Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu

1960                    1970                    1980                    1990                    2000  
 |                    |                    |                    |                    |  
 CAA GGT AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG  
 Gln Gly Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu

2010                    2020                    2030                    2040  
 |                    |                    |                    |  
 GGG ATT GAG GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT  
 Gly Ile Glu Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala

2050                    2060                    2070                    2080                    2090  
 |                    |                    |                    |                    |  
 CAA ACC AGT TTA GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG  
 Gln Thr Ser Leu Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu

2100                    2110                    2120                    2130  
 |                    |                    |                    |  
 CGT GGC ATT GTG TTA TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG  
 Arg Gly Ile Val Leu Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln

2140                    2150                    2160                    2170                    2180  
 |                    |                    |                    |                    |  
 AAA ACT AAA GCA GGC CAA GCA TTA GGT TCT GCC GAA AGC ATT GTA  
 Lys Thr Lys Ala Gly Gln Ala Leu Gly Ser Ala Glu Ser Ile Val

2190                    2200                    2210                    2220  
 |                    |                    |                    |  
 CAA AAT GCA AAT AAA GCC AAA ACT GTA TTA TCT GGC ATT CAA TCT  
 Gln Asn Ala Asn Lys Ala Lys Thr Val Leu Ser Gly Ile Gln Ser

2230                    2240                    2250                    2260                    2270  
 |                    |                    |                    |                    |  
 ATT TTA GGC TCA GTA TTG GCT GGA ATG GAT TTA GAT GAG GCC TTA  
 Ile Leu Gly Ser Val Leu Ala Gly MET Asp Leu Asp Glu Ala Leu

FIG. 15A

2280                      2290                      2300                      2310  
 CAG AAT AAC AGC AAC CAA CAT GCT CTT GCT AAA GCT GGC TTG GAG  
 Gln Asn Asn Ser Asn Gln His Ala Leu Ala Lys Ala Gly Leu Glu

2320                      2330                      2340                      2350                      2360  
 CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT AAT TCA GTA AAA ACA  
 Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala Asn Ser Val Lys Thr

2370                      2380                      2390                      2400  
 CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT GGT TCA AAA CTA  
 Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe Gly Ser Lys Leu

2410                      2420                      2430                      2440                      2450  
 CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA CTC AAA AAT  
 Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys Leu Lys Asn

2460                      2470                      2480                      2490  
 ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT ATC TCA  
 Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val Ile Ser

2500                      2510                      2520                      2530                      2540  
 GGG CTA TTA TCG GGC GCA ACC GCT GCA CTT GTA CTT GCA GAT AAA  
 Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp Lys

2550                      2560                      2570                      2580  
 AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA  
 Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala

2590                      2600                      2610                      2620                      2630  
 AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT  
 Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile

2640                      2650                      2660                      2670  
 TTA GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG  
 Leu Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val

FIG. 15B

2680            2690            2700            2710            2720  
 GCT GCT TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA  
 Ala Ala Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu  
  
 2730            2740            2750            2760  
 GCA TTT GCC GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA  
 Ala Phe Ala Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu  
  
 2770            2780            2790            2800            2810  
 GAG AGT TAT GCC GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT  
 Glu Ser Tyr Ala Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp  
  
 2820            2830            2840            2850  
 AAT TTA TTA GCA GAA TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA  
 Asn Leu Leu Ala Glu Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala  
  
 2860            2870            2880            2890            2900  
 TCG GTT ACT GCA ATT AAT ACC GCA TTG GCC GCT ATT GCT GGT GGT  
 Ser Val Thr Ala Ile Asn Thr Ala Leu Ala Ala Ile Ala Gly Gly  
  
 2910            2920            2930            2940  
 GTG TCT GCT GCT GCA GCC GAT TTA ACA TTT GAA AAA GTT AAA CAT  
 Val Ser Ala Ala Ala Ala Asp Leu Thr Phe Glu Lys Val Lys His  
  
 2950            2960            2970            2980            2990  
 AAT CTT GTC ATC ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA  
 Asn Leu Val Ile Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln  
  
 3000            3010            3020            3030  
 AAC TGG TTC CGA GAG GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT  
 Asn Trp Phe Arg Glu Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr  
  
 3040            3050            3060            3070            3080  
 AAA GCA ACT AAA GAT GAG AAA ATC GAA GAA ATC ATC GGT CAA AAT  
 Lys Ala Thr Lys Asp Glu Lys Ile Glu Glu Ile Ile Gly Gln Asn

FIG. 15C

3090	3100	3110	3120	
GGC GAG CGG ATC ACC TCA AAG CAA GTT GAT GAT CTT ATC GCA AAA				
Gly Glu Arg Ile Thr Ser Lys Gln Val Asp Asp Leu Ile Ala Lys				
3130	3140	3150	3160	3170
GGT AAC GGC AAA ATT ACC CAA GAT GAG CTA TCA AAA GTT GTT GAT				
Gly Asn Gly Lys Ile Thr Gln Asp Glu Leu Ser Lys Val Val Asp				
3180	3190	3200	3210	
AAC TAT GAA TTG CTC AAA CAT AGC AAA AAT GTG ACA AAC AGC TTA				
Asn Tyr Glu Leu Leu Lys His Ser Lys Asn Val Thr Asn Ser Leu				
3220	3230	3240	3250	3260
GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT ACC TCG TCT AAT GAT				
Asp Lys Leu Ile Ser Ser Val Ser Ala Phe Thr Ser Ser Asn Asp				
3270	3280	3290	3300	
TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG TTG GAT CAA AGT				
Ser Arg Asn Val Leu Val Ala Pro Thr Ser <u>MET</u> Leu Asp Gln Ser				
3310	3320	3330	3340	
TTA TCT TCT CTT CAA TTT GCT AGG <u>GGA TCC</u> TAG				
Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser ---				

FIG. 15D

1 ATGCAAAAAC TGCAAATCTC TGTTTATATT TACCTATTTA CGCTGATTGT  
 51 TGCTGGCCCA GTGGATCTGA ATGAGAACAG CGAGCAGAAG GAAAATGTGG  
 101 AAAAAGAGGG GCTGTGTAAT GCATGTTTGT GGAGGGAAAA CACTACATCC  
 151 TCAAGACTAG AAGCCATAAA AATCCAAATC CTCAGTAAAC TTCGCCTGGA  
 201 AACAGCTCCT AACATCAGCA AAGATGCTAT CAGACAACTT TTGCCCAAGG  
 251 CTCCTCCACT CCTGGAAGTG ATTGATCAGT TCGATGTCCA GAGAGATGCC  
 301 AGCAGTGACG GCTCCTTGGA AGACGATGAC TACCACGCCA GGACGGAAAC  
 351 GGTCAATTACC ATGCCCACGG AGTCTGATCT TCTAACGCAA GTGGAAGGAA  
 401 AACCCAAATG TTGCTTCTTT AAATTTAGCT CTAAGATACA ATACAATAAA  
 451 CTAGTAAAGG CCCAACTGTG GATATATCTG AGGCCTGTCA AGACTCCTGC  
 501 GACAGTGTTT GTGCAAATCC TGAGACTCAT CAAACCCATG AAAGACGGTA  
 551 CAAGGTATAC TGAATCCGA TCTCTGAAAC TTGACATGAA CCCAGGCACT  
 601 GGTATTTGGC AGAGCATTGA TGTGAAGACA GTGTTGCAGA ACTGGCTCAA  
 651 ACAACCTGAA TCCAACCTAG GCATTGAAAT CAAAGCTTTA GATGAGAATG  
 701 GCCATGATCT TGCTGTAACC TTCCCAGAAC CAGGAGAAGA TGGACTGACT  
 751 CCTTTTTTAG AAGTCAAGGT AACAGACACA CAAAAAGAT CTAGGAGAGA  
 801 TTTTGGGCTT GATTGTGATG AACACTCCAC AGAATCTCGA TGCTGTCGCT  
 851 ACCCCCTCAC GGTGGATTTT GAAGCTTTTG GATGGGATTG GATTATTGCA  
 901 CCTAAAAGAT ATAAGGCCAA TTA CTGCTCT GGAGAATGTG AATTTGTATT  
 951 TTTGCAAAAG TATCCTCATA CCCATCTTGT GCACCAAGCA AACCCAGAG  
 1001 GTTCAGCCGG CCCCTGCTGT ACTCCTACAA AGATGTCTCC AATTAATATG  
 1051 CTATATTTTA ATGGCGAAGG ACAAATAATA TACGGGAAGA TTCCAGCCAT  
 1101 GGTAGTAGAT CGCTGTGGGT GCTCATGA

FIG. 16A

1 MQKLQISVYI YLFTLIVAGP VDLNENSEQK ENVEKEGLCN ACLWRENTTS  
 51 SRLEAIKIQI LSKLRLETAP NISKDAIRQL LPKAPLLEL IDQFDVQRDA  
 101 SSDGSLEDDD YHARTETVIT MPTESDLLTQ VEGKPKCCFF KFSSKIQYNK  
 151 LVKAQLWIYL RPKVTPATVF VQILRLIKPM KDGTRYTGIR SLKLDMNPGT  
 201 GIWQSIDVKT VLQNLWKQPE SNLGIEIKAL DENGHD LAVT FPEPGEDGLT  
 251 PFLEVKVTD T PKRSRRDFGL DCDEHSTESR CCRYPLTVDF EAFGWDWIIA  
 301 PKRYKANYCS GECEFVFLQK YPHTHLVHQA NPRGSAGPCC TPTKMSPINM  
 351 LYFN GEGQII YGKIPAMVVD RCGCS

FIG. 16B

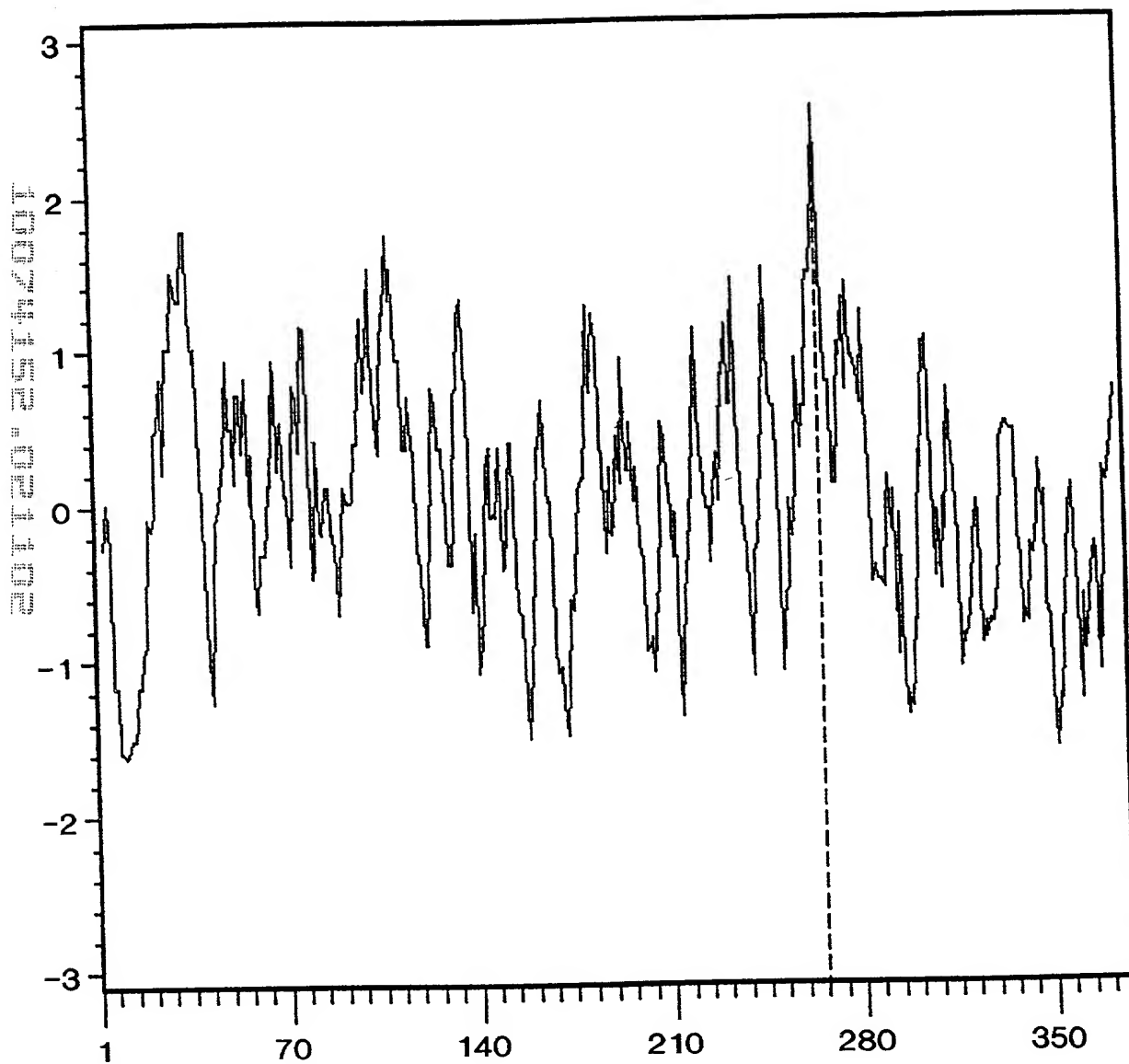


FIG. 17



and the other in the other half of the group.

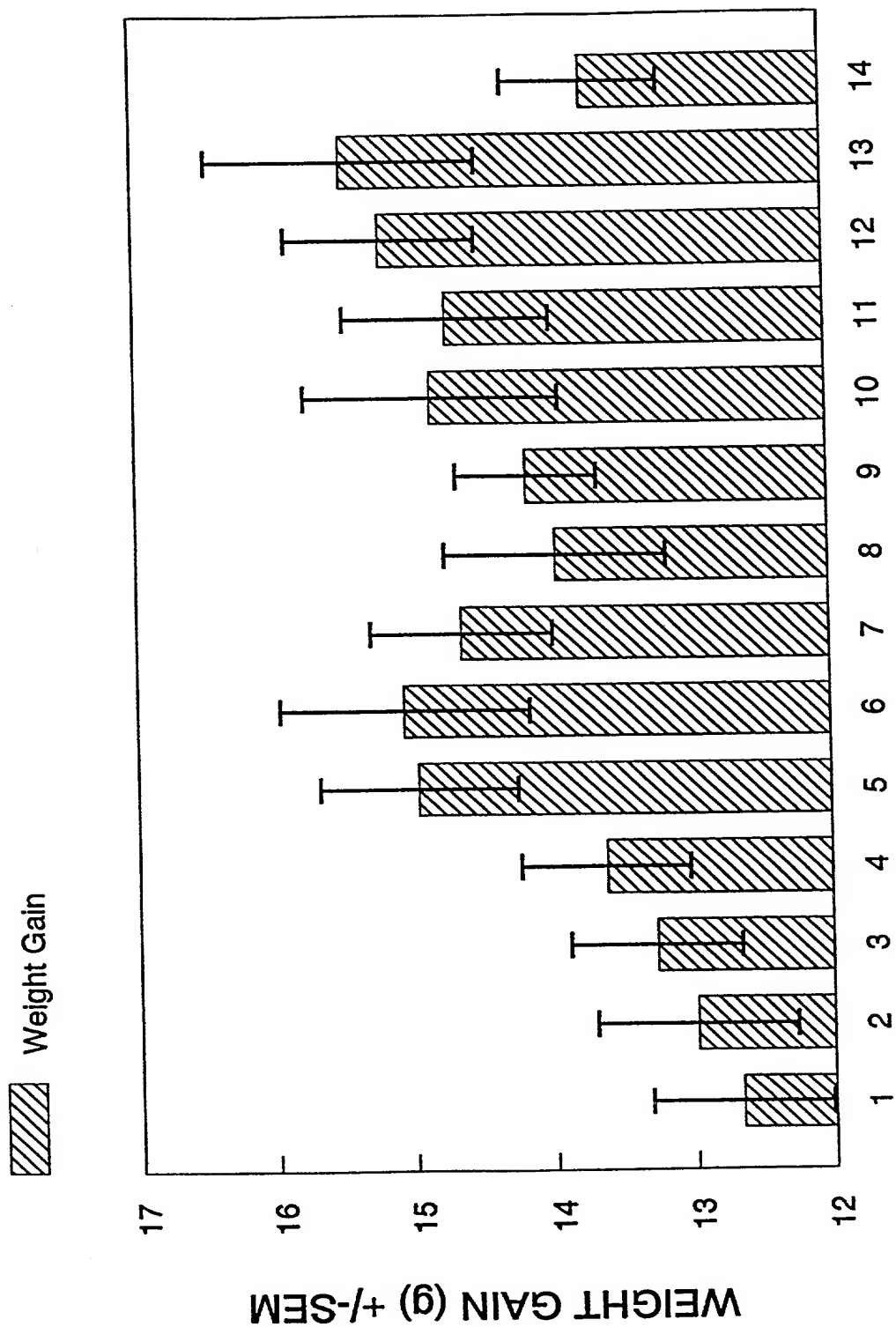


FIG. 18